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Marker assisted breeding in sugar beet design and evaluation of molecular markers targeting early flowering

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Marker assisted breeding in sugar beet: design and evaluation of molecular markers targeting early flowering

Houda KHAMIS

A dissertation in partial fulfillment of the requirements for the
degree of PhD in Biological Sciences

Supervisor: Pr. Pierre VAN CUTSEM

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Faculty of Sciences
DEPARTMENT OF BIOLOGY
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Marker assisted breeding in sugar beet: design and evaluation of molecular markers targeting early flowering

By Houda Khamis

Beta vulgaris is a biennial plant, which under both vernalization and long photoperiods, shows early flowering during the first growing year. Early flowering of sugar beet results in a reduction of sugar yields. Despite systematic phenotypic counter-selection, early flowering plants are still observed in the fields.

The aim of this work was to identify sequence polymorphisms statistically associated with early flowering in sugar beet so they can be used to develop new molecular markers. These markers would contribute to improve breeding and selection for sugar beet varieties more resistant to early flowering.

To reach this goal, we followed a candidate gene approach relying on the extensive knowledge of flowering time control available on the model species *Arabidopsis thaliana*. In our strategy, we first isolated homologous genes related to flowering time control in sugar beet, we then studied their polymorphisms by performing EcoTILLING in contrasted samples originating from the same cultivar (Angeliqua). We finally looked for putative association between the identified genetic polymorphisms and the early flowering phenotype.

At the end of this research, we were able to identify SNP and indel polymorphisms in *BvGI*, *BvSUF4*, *BvPHYB*, *BvPHYA*, *BvFT1*, *BvCRY1*, *BvFY* and *BvTINYL2* genes. Following the genotyping of two sets of contrasted sugar beet plants with PAMSA probes, statistically significant associations were confirmed between detected polymorphisms within *BvGI*, *BvSUF4*, *BvPHYB*, *BvTINYL2* genes and the early flowering phenotype.

In conclusion, the candidate gene approach proved to be a promising method to investigate phenotype / genotype association in sugar beet. Four promising targets were identified in this study. These results might favor the development of improved varieties of sugar beet.

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